

## EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L5	16656	Ruben.IN. or Baker.IN. or Ni.IN.	US-PGPUB; USPAT	OR	ON	2006/09/01 17:25
L6	5	L5 and TR20	US-PGPUB; USPAT	OR	ON	2006/09/01 17:25

This page gives you Search Results detail for the Application 10618797 and Search Result us-10-618-797-2.ra1.

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OM protein - protein search, using sw model

Run on: August 1, 2006, 11:36:35 ; Search time 26 Seconds  
(without alignments)  
478.052 Million cell updates/sec

Title: US-10-618-797-2 -  
Perfect score: 803  
Sequence: 1 MRSCPEEQYWAALLGTCMFC.....FPQLPPTQLSGLGPNIGLL 142

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	803	100.0	142	2	US-09-848-295-2	Sequence 2, Appli
2	195	24.3	293	1	US-08-810-572A-2	Sequence 2, Appli
3	195	24.3	293	2	US-09-290-333-2	Sequence 2, Appli
4	195	24.3	293	2	US-09-782-857A-2	Sequence 2, Appli
5	195	24.3	293	2	US-09-879-919-22	Sequence 22, Appli
6	195	24.3	293	2	US-09-848-295-4	Sequence 4, Appli
7	195	24.3	293	2	US-09-854-864-14	Sequence 14, Appli
8	195	24.3	293	2	US-09-961-376-2	Sequence 2, Appli
9	192.5	24.0	166	1	US-08-810-572A-6	Sequence 6, Appli

10	192.5	24.0	166	2	US-09-290-333-6	Sequence 6, Appli
11	192.5	24.0	166	2	US-09-782-857A-6	Sequence 6, Appli
12	192.5	24.0	166	2	US-09-854-864-15	Sequence 15, Appl
13	192.5	24.0	397	2	US-09-854-864-18	Sequence 18, Appl
14	180.5	22.5	67	2	US-09-854-864-16	Sequence 16, Appl
15	172.5	21.5	59	2	US-09-854-864-20	Sequence 20, Appl
16	95.5	11.9	299	2	US-09-286-529-17	Sequence 17, Appl
17	95	11.8	211	2	US-09-286-529-20	Sequence 20, Appl
18	95	11.8	271	2	US-09-936-019-1	Sequence 1, Appli
19	95	11.8	271	2	US-09-936-024-1	Sequence 1, Appli
20	95	11.8	300	1	US-08-794-796-2	Sequence 2, Appli
21	95	11.8	300	2	US-09-632-277A-2	Sequence 2, Appli
22	95	11.8	300	2	US-09-523-323-52	Sequence 52, Appl
23	95	11.8	300	2	US-09-896-096A-1	Sequence 1, Appli
24	95	11.8	300	2	US-09-936-019-3	Sequence 3, Appli
25	95	11.8	300	2	US-09-936-024-3	Sequence 3, Appli
26	95	11.8	333	2	US-09-949-016-7678	Sequence 7678, Ap
27	94	11.7	258	2	US-09-579-845-9	Sequence 9, Appli
28	94	11.7	474	1	US-08-650-000-4	Sequence 4, Appli
29	94	11.7	474	2	US-09-042-785A-8	Sequence 8, Appli
30	94	11.7	474	2	US-09-758-124-4	Sequence 4, Appli
31	94	11.7	474	7	5395760-4	Patent No. 5395760
32	88.5	11.0	351	2	US-09-270-767-42774	Sequence 42774, A
33	86	10.7	146	2	US-09-523-323-59	Sequence 59, Appl
34	86	10.7	153	2	US-09-286-529-2	Sequence 2, Appli
35	85	10.6	589	1	US-07-668-648-6	Sequence 6, Appli
36	85	10.6	589	1	US-08-429-998-6	Sequence 6, Appli
37	85	10.6	589	1	US-08-431-333-6	Sequence 6, Appli
38	85	10.6	589	2	US-08-991-862-2	Sequence 2, Appli
39	85	10.6	589	2	US-09-813-156-2	Sequence 2, Appli
40	85	10.6	589	2	US-09-456-886-2	Sequence 2, Appli
41	85	10.6	589	2	US-09-824-647-2	Sequence 2, Appli
42	85	10.6	589	2	US-09-880-842-2	Sequence 2, Appli
43	85	10.6	589	5	PCT-US91-02321-6	Sequence 6, Appli
44	83.5	10.4	258	2	US-09-579-845-7	Sequence 7, Appli
45	83.5	10.4	487	2	US-09-579-845-14	Sequence 14, Appl

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OM protein - protein search, using sw model

Run on: August 1, 2006, 11:48:04 ; Search time 181 Seconds  
(without alignments)  
363.406 Million cell updates/sec

Title: US-10-618-797-2  
Perfect score: 803  
Sequence: 1 MRSCPEEQYWAALLGTCMFC.....FPQLPPTQLSGLGPNIGGLL 142

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_Main:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	803	100.0	142	4	US-10-618-797-2
2	199.5	24.8	292	5	US-10-967-527A-19
3	198.5	24.7	291	3	US-09-779-050A-43
4	198	24.7	293	3	US-09-779-050A-42
5	195	24.3	245	6	US-11-200-992-9
6	195	24.3	265	5	US-10-626-914-17
7	195	24.3	265	5	US-10-485-489-19
8	195	24.3	265	5	US-10-861-049-36
9	195	24.3	265	6	US-11-021-874-36
10	195	24.3	265	6	US-11-069-473-9

11	195	24.3	293	3	US-09-879-919-22	Sequence 22, Appl
12	195	24.3	293	3	US-09-854-864-14	Sequence 14, Appl
13	195	24.3	293	3	US-09-855-158-14	Sequence 14, Appl
14	195	24.3	293	3	US-09-961-376-2	Sequence 2, Appli
15	195	24.3	293	3	US-09-302-863-2	Sequence 2, Appli
16	195	24.3	293	3	US-09-855-564-2	Sequence 2, Appli
17	195	24.3	293	4	US-10-087-192-1650	Sequence 1650, Ap
18	195	24.3	293	4	US-10-084-971-2	Sequence 2, Appli
19	195	24.3	293	4	US-10-068-725-4	Sequence 4, Appli
20	195	24.3	293	4	US-10-151-882-46	Sequence 46, Appl
21	195	24.3	293	4	US-10-293-816-2	Sequence 2, Appli
22	195	24.3	293	4	US-10-008-063-8	Sequence 8, Appli
23	195	24.3	293	4	US-10-152-363A-2	Sequence 2, Appli
24	195	24.3	293	4	US-10-268-951-22	Sequence 22, Appl
25	195	24.3	293	4	US-10-258-368-1	Sequence 1, Appli
26	195	24.3	293	4	US-10-618-797-4	Sequence 4, Appli
27	195	24.3	293	4	US-10-742-634-7	Sequence 7, Appli
28	195	24.3	293	4	US-10-748-112-27	Sequence 27, Appl
29	195	24.3	293	5	US-10-684-149-4	Sequence 4, Appli
30	195	24.3	293	5	US-10-626-914-3	Sequence 3, Appli
31	195	24.3	293	5	US-10-485-489-3	Sequence 3, Appli
32	195	24.3	293	5	US-10-861-049-25	Sequence 25, Appl
33	195	24.3	293	5	US-10-742-634-7	Sequence 7, Appli
34	195	24.3	293	6	US-11-021-874-25	Sequence 25, Appl
35	195	24.3	293	6	US-11-079-418-2	Sequence 2, Appli
36	195	24.3	293	6	US-11-221-849-2	Sequence 2, Appli
37	195	24.3	293	6	US-11-242-294-2	Sequence 2, Appli
38	195	24.3	293	6	US-11-200-992-6	Sequence 6, Appli
39	195	24.3	293	6	US-11-069-473-2	Sequence 2, Appli
40	195	24.3	301	4	US-10-258-368-12	Sequence 12, Appl
41	193	24.0	344	4	US-10-152-363A-52	Sequence 52, Appl
42	193	24.0	344	6	US-11-242-294-52	Sequence 52, Appl
43	192.5	24.0	166	3	US-09-854-864-15	Sequence 15, Appl
44	192.5	24.0	166	3	US-09-855-158-15	Sequence 15, Appl
45	192.5	24.0	166	4	US-10-293-816-6	Sequence 6, Appli

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OM protein - protein search, using sw model

Run on: August 1, 2006, 11:48:34 ; Search time 31 Seconds  
(without alignments)  
302.525 Million cell updates/sec

Title: US-10-618-797-2  
Perfect score: 803  
Sequence: 1 MRSCPEEQYWAALLGTCMFC.....FPQLPPTQLSGLGPNIGLL 142

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 232337 seqs, 66044171 residues

Total number of hits satisfying chosen parameters: 232337

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_New:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*  
8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	195	24.3	293	7	US-11-318-156-2	Sequence 2, Appli
2	192.5	24.0	166	7	US-11-318-156-6	Sequence 6, Appli
3	94	11.7	258	6	US-10-643-589-4	Sequence 4, Appli
4	82	10.2	408	7	US-11-175-714-140	Sequence 140, App
5	82	10.2	430	6	US-10-539-228-522	Sequence 522, App
6	82	10.2	430	7	US-11-175-714-138	Sequence 138, App
7	81.5	10.1	41	7	US-11-272-521-196	Sequence 196, App
8	81.5	10.1	810	6	US-10-781-841-34	Sequence 34, Appl

9	79	9.8	367	7	US-11-056-355B-5843	Sequence 5843, Ap
10	79	9.8	374	7	US-11-056-355B-5842	Sequence 5842, Ap
11	79	9.8	417	7	US-11-056-355B-5841	Sequence 5841, Ap
12	78.5	9.8	1373	7	US-11-105-233-187	Sequence 187, App
13	78.5	9.8	1934	7	US-11-174-307B-1742	Sequence 1742, Ap
14	77	9.6	673	6	US-10-449-902-55530	Sequence 55530, A
15	77	9.6	1144	7	US-11-174-307B-2720	Sequence 2720, Ap
16	76.5	9.5	2124	7	US-11-283-329-160	Sequence 160, App
17	76	9.5	330	7	US-11-293-697-4511	Sequence 4511, Ap
18	76	9.5	417	6	US-10-505-928-793	Sequence 793, App
19	76	9.5	876	7	US-11-174-307B-144	Sequence 144, App
20	76	9.5	1097	7	US-11-174-307B-1420	Sequence 1420, Ap
21	76	9.5	1136	7	US-11-174-307B-2400	Sequence 2400, Ap
22	76	9.5	1408	7	US-11-174-307B-2196	Sequence 2196, Ap
23	76	9.5	1601	7	US-11-174-307B-2364	Sequence 2364, Ap
24	75.5	9.4	1401	7	US-11-174-307B-764	Sequence 764, App
25	75.5	9.4	1444	7	US-11-174-307B-2626	Sequence 2626, Ap
26	75.5	9.4	1445	7	US-11-174-307B-1452	Sequence 1452, Ap
27	75.5	9.4	1552	7	US-11-174-307B-1110	Sequence 1110, Ap
28	75.5	9.4	3291	7	US-11-174-307B-2666	Sequence 2666, Ap
29	75	9.3	72	6	US-10-449-902-50808	Sequence 50808, A
30	75	9.3	954	7	US-11-174-307B-2028	Sequence 2028, Ap
31	75	9.3	1304	7	US-11-174-307B-2586	Sequence 2586, Ap
32	75	9.3	1305	7	US-11-174-307B-2140	Sequence 2140, Ap
33	75	9.3	1315	7	US-11-174-307B-4248	Sequence 4248, Ap
34	74.5	9.3	1056	7	US-11-174-307B-1808	Sequence 1808, Ap
35	74.5	9.3	1353	7	US-11-174-307B-66	Sequence 66, Appl
36	74.5	9.3	1689	7	US-11-174-307B-1196	Sequence 1196, Ap
37	74.5	9.3	1980	7	US-11-174-307B-1298	Sequence 1298, Ap
38	74	9.2	1077	7	US-11-174-307B-1630	Sequence 1630, Ap
39	74	9.2	1549	7	US-11-174-307B-608	Sequence 608, App
40	73.5	9.2	121	6	US-10-374-780A-2152	Sequence 2152, Ap
41	73.5	9.2	931	7	US-11-174-307B-2082	Sequence 2082, Ap
42	73.5	9.2	1263	7	US-11-174-307B-1510	Sequence 1510, Ap
43	73.5	9.2	1355	7	US-11-174-307B-2278	Sequence 2278, Ap
44	73.5	9.2	1708	7	US-11-174-307B-2086	Sequence 2086, Ap
45	73	9.1	260	6	US-10-511-937-2519	Sequence 2519, Ap